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EXAMINER	
SPECTOR, LORRAINE	
ART UNIT	**PAPER NUMBER**
1647	

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
3 MONTHS	12/21/2006	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

Office Action Summary	Application No.	Applicant(s)	
	09/991,163	ASHKENAZI ET AL.	
	Examiner	Art Unit	
	Lorraine Spector, Ph.D.	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *29 September 2006*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *124-126 and 129-133* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *124,126 and 131-133* is/are rejected.

7)☒ Claim(s) *125, 129* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *9/29/06*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

Detailed Office Action

Claims 124-126 and 129-133 are pending and under consideration. The claims are drawn to PRO1111 protein. The claims have been amended to remove reference to "the extracellular domain", and to "native sequence".

The rejection of claims 124, 132 and 133 under 35 U.S.C. §112, first paragraph on the basis of lack of adequate written description of a transmembrane domain is withdrawn in view of applicants amendments to the claims to remove reference to such. However, the remainder of the rejection is maintained, see below.

Information Disclosure Statement

The information disclosure statement, filed 9/29/06, has been considered.

Priority Determination

The utility for the claimed protein is active in a chondrocyte redifferentiation assay. Applicants have established that the PCT application contains the chondrocyte redifferentiation. Accordingly, priority is set at 3/30/00.

Applicants have once again argued in the paper filed 9/29/2006 that priority is merited to at least June 23, 1999 on the basis of gene amplification. This argument has been fully considered but is not deemed persuasive for reasons cited below:

To reiterate applicants previous argument (since the instant arguments are not specific about *what* utility is being asserted), applicants reiterate the argument that amplification of the *gene* encoding the claimed proteins in seven lung tumors and four colon tumors establishes that it is more likely than not that the claimed protein can be used as a cancer diagnostic. This argument has been fully considered but is not deemed persuasive because it is an incomplete and misleading characterization of the data in the specification. According to the specification at page 552-553, seven of nineteen lung tumor cell lines and four of seventeen colon tumor cell lines tested positive. However, it remains that the amplification was minimal, and that the most

parsimonious explanation is aneuploidy, with no evidence that the chromosome bearing PRO1111 was preferentially amplified (as opposed to other chromosomes). Aneuploidy is also a feature of damaged tissue, and is commonly found in colon and lung tissues, which are subject to environmental damage. It does not invariably or inevitably lead to cancer; rather, such damaged cells are generally removed by the body via apoptosis; the development of cancer is the exception, as evidenced by the fact that the general population is constantly suffering damage to lung cells via air pollution, whereas lung cancer remains relatively rare. Further, it remains that the 2-3 fold amplification of the nucleic acid is consistent with a simple case of aneuploidy, in which there is a single extra copy of the chromosome in question, and is *not* predictive of a similar differential in protein expression; hence, the argument is not persuasive, as the claims are drawn to polypeptides, not the nucleic acids that encode them. Merely because amplification *may* be an *initial* step in the formation of cancer does not equate with a substantial assertion of diagnostic utility for the encoded protein. There is no factual support for applicant's assertion at the bottom of page 5 of the response that "it helps in identifying individuals at *significantly increased cancer risk" (*emphasis added).

At page 5 of the response filed 9/29/2006, applicants argue that they are not required to establish a necessary correlation between gene amplification and protein levels, but merely that a preponderance of the totality of evidence is required. The Examiner takes no issue with this premise, and maintains that the preponderance of the totality of the evidence points to lack of predictability, and in fact, in view of the references newly cited by applicants, argues *against* such a correlation existing, as discussed below.

The first Polakis declaration has been fully considered on the record, and does not require further discussion, in and of itself.

Applicants have submitted a second Polakis declaration, filed 9/29/2006, signed 3/29/2006, which is discussed at pages 4-5 of the response.

In assessing the weight to be given expert testimony, the examiner may properly consider, among other things, the nature of the fact sought to be established, the strength of any opposing evidence, the interest of the expert in the outcome of the case, and the presence or absence of factual support for the expert's opinion. See Ex parte Simpson, 61 USPQ2d 1009 (BPAI 2001), Cf. Redac Int'l. Ltd. v. Lotus Development Corp., 81 F.3d 1576, 38 USPQ2d 1665

(Fed. Cir. 1996), Paragon Podiatry Lab., Inc. v. KLM Lab., Inc., 948 F.2d 1182, 25 USPQ2d 1561, (Fed. Cir. 1993).

Affidavits or declarations are provided as evidence and must set forth facts, not merely conclusions. In re Pike and Morris, 84 USPQ 235 (CCPA 1949).

The Polakis II declaration has been fully considered to the following effect:

In the instant case, the nature of the fact sought to be established is whether or not gene amplification is predictive of increased mRNA levels and, in turn, increased protein levels. (1) Dr. Polakis declares that 28 of 31genes identified as being detectably over expressed at the mRNA level were found also to have increased protein levels. (2) It is important to note that the instant specification only discloses gene amplification data for PRO1111 (i.e., data regarding amplification of PRO1111 genomic DNA), and does not disclose any information regarding PRO1111 mRNA levels. This was the main issue with the first Polakis declaration, and remains pertinent; there is no demonstration of *any* mRNA level for PRO1111, hence the theoretical correlation of mRNA with protein is not probative. The fact that needs to be established here is that a ΔCt value of at least 1.0 would be predictive of increased protein expression. Applicants have never addressed this point directly. Furthermore, there is strong opposing evidence showing that *gene amplification is not predictive of increased mRNA levels* in normal and cancerous tissues See, e.g., Pennica et al., discussed in the Examiner's Answer. (3) Regarding the interest of the expert in the outcome of the case, it is noted that Dr. Polakis is employed by the assignee. (4) Finally, Dr. Polakis refers to facts; however, the data refer to the mRNA's in question only by UNQ numbers; UNQ419, which is PRO1111, is not represented, and declarant provides no information about the sequences that *are* represented; the assertion in the specification is that PRO1111 had a for 2/9 primary lung adenocarcinoma cell lines, 5/11 primary lung squamous cell carcinomas, and 13/17 colon adenocarcinoma. It is not clear whether any or all of these tissues were represented in the data. There is no indication of *how much* the mRNA and protein were overexpressed, as there is no actual description of the experiment that was done, but rather a conclusory statement as to what was measured, and what it means.

For the reasons above, the Polakis II declaration is not sufficient to overcome the rejection of claims 58-62 under 35 U.S.C. §101 and §112, second paragraph.

The Examiner notes that the two Polakis declarations are not consistent:

In the first declaration, Dr. Polakis declares that "we have identified approximately 200 gene transcripts that are present in human tumor cells at significantly higher levels than in corresponding normal human cells". In the second, he states that "we have identified approximately 200 gene transcripts that are present in human tumor ***tissue*** at significantly higher levels than in corresponding normal human ***tissue***."

In the first declaration, Dr. Polakis declares that "In approximately 80% of our observations we have found that increases in the level of a particular mRNA correlates with changes in the level of protein expressed from that mRNA when human tumor cells are compared with their corresponding normal cells." In the second, he states that "of the 31 genes identified as being detectably overexpressed in human tumor tissue as compared to normal human tissue at the mRNA level, 28 of them (i.e. greater than 90%) are also detectably overexpressed in human tumor tissue as compared to normal human tissue at the protein level."

It cannot be determined whether the two declarations are referring to the same data set, or different data sets. Further, there has been no explanation of why the Declarant now refers to tumor *tissue* rather than tumor *cells,* nor what the perceived significance of this change is.

In the Response of 9/26/2006, Applicant has submitted teachings from Alberts, B. (Molecular Biology of the Cell (3rd ed 1994 and 4th ed 2002)) and Lewin, B. (Genes VI 1997) to support the statements of Dr. Polakis (Polakis II declaration; (see above). Applicant also cites numerous references to emphasize that those of skill in the art would not be focusing on differences in gene expression between cancer cells and normal cells if there were no correlation between gene expression and protein expression (such as Zhigang et al., Meric et al. Ornoft et al., Wang et al., Munaut et al., Hui et al., Khal et al., Maruyama et6 al., Caberlotto et al., Misrachi et al., Stein et al., Gou et al., etc.). Applicant asserts that changes in mRNA level generally lead to corresponding changes in the level of expressed protein. Applicant also contends that the references and the Polakis declaration establish that the accepted understanding

in the art is that there is a reasonable correlation between changes in gene expression and the level of the encoded protein.

Applicant's arguments have been fully considered but are not found to be persuasive. While the Examiner acknowledges the teachings of Alberts and Lewin, which disclose that initiation of transcription is the most common point for a cell to regulate the gene expression, it is not the only means of regulating gene expression. For example, Alberts also teaches that there are a number of other controls that can act later in the pathway from RNA to protein to modulate the amount of protein that is made, including translational control mechanisms and mRNA degradation control mechanisms (see Alberts 3rd ed., bottom of pg 453). Meric et al. states the following:

"The fundamental principle of molecular therapeutics in cancer is to exploit the differences in gene expression between cancer cells and normal cells. [M]ost efforts have concentrated on identifying differences in gene expression at the level or mRNA, which can be attributable to either DNA amplification or to differences in transcription."

However, Meric et al. also goes on to state that gene expression is quite complicated, and is also regulated at the level of mRNA stability, mRNA translation, and protein stability (see page 971, Introduction). Meric et al. also teaches that there are a number of translation alterations encountered in cancer, including variations in the mRNA sequence as a result of mutations, alternate splicing and transcription start sites, alternate polyadenylation sites, and alterations in the components of the translation machinery (see pages 973-974). Celis et al. also teach that "[g]enes may be present, they may be mutated, but they are not necessarily transcribed. Some messengers are transcribed but not translated, and the number of mRNA copies does not necessarily reflect the number of functional protein molecules" (pg 6, col 2).

Applicants have submitted a voluminous new information disclosure statement, with 149 reference, purportedly to show that genomic DNA, as measured for PRO1111, is predictive of protein levels. A number of applicants arguments continue to be, and the vast majority of newly cited references are, directed at the predictability of protein levels when *mRNA* levels are amplified. The Examiner maintains that the most significant issue in this case is that the data are drawn to *genomic* data, and *not* mRNA data. While the Examiner concedes that if *mRNA* levels were shown to be significantly higher in a significant proportion of a given tumor type that such

would be indicative of utility for the claimed protien, she maintains that such is not predictable based upon the data in the specification, which are specifically drawn to amplification of *genomic* DNA.

While the vast majority of newly cited references are drawn to predictability of protein on the basis of mRNA amplification (and for reasons cited above do not merit further discussion), a single reference, that by Godbout, is pertinent to the issue at hand. However, the Examiner finds applicants interpretation of the reference to be erroneous. Far from teaching predictability for expression of PRO1111 on the basis of a minor genomic amplification, the abstract of Godbout teaches "The DEAD box gene, DDX1, is a putative RNA helicase that is co-amplified with MYCN in a subset of retinoblastoma (RB) and neuroblastoma (NB) tumors and cell lines. Although gene amplification usually involves hundreds to thousands of kilobase pairs of DNA, a number of studies suggest that co-amplified genes are only overexpressed if they provide a selective advantage to the cells in which they are amplified." The protein encoded by the DDX gene *had been characterized* as being a putative RNA helicase, a type of enzyme that *would be expected to confer a selective advantage* to the cells in which it (the DDX gene) was amplified. On page 21167, right column, first full paragraph, Godbout et al. state "*It is generally accepted that co-amplified genes are not over-expressed unless they provide a selective growth advantage to the cell* (48, 49). For example, although ERBA is closely linked to ERBB2 in breast cancer and both genes are commonly amplified in these tumors, ERBA is not overexpressed (48). Similarly, three genes mapping to 12q13-14 (CDK4, SAS and MDM2) are overexpressed in a high percentage of malignant gliomas showing amplification of this chromosomal region, while other genes mapping to this region (GADD153, GL1, and A2MR) are rarely overexpressed in gene-amplified malignant gliomas (50, 51). The first three genes are probably the main targets of the amplification process, while the latter three genes are probably incidentally included in the amplicons."

On the contrary, there is no structure/function analysis in the specification regarding the putative protein encoded by the PRO1111 gene. It is not disclosed, and based upon the sequence searches in this case, the Examiner cannot find any reason to suspect, that the protein encoded by the PRO1111 gene would confer any selective advantage on a cell expressing it. It has no known homology to an RNA helicase or any other protein that would be expected to confer a selective

advantage to a tumor cell. Further, it cannot be determined from the abstract whether the level of genomic amplification of the DDX1 gene was comparable to that disclosed for PRO1111.

An additional reference that provides evidence that gene amplification does not predictably or even predominantly lead to increased transcript is Li et al., Oncogene, Vol. 25, pages 2628-2635, 2006. Li et al. used a functional approach that integrated simultaneous genomic and transcript microarray, proteomics, and tissue microarray analyses to directly identify putative oncogenes in lung adenocarcinoma. On page 2633, right column, Li et al. state: "*In our study, 68.8% of the genes showing over-representation in the genome did not show elevated transcript levels*, implying that at least some of these genes are 'passenger' genes that are concurrently amplified because of their location with respect to amplicons but *lack biological relevance in terms of the development of lung adenocarcinoma*."

In summary, of applicants 149 references submitted (not 148, as stated by applicants), only a single one, Godbout, is drawn to the predictability of protein levels based upon genomic DNA amplification, and that one supports the Examiners assertion that it is more likely than not that the PRO1111 protein would *not* be expected to be found in increased amounts in the cells tested by applicants, and thus has no utility as a cancer diagnostic.

It remains that the art considers that that gene amplification does not reliably correlate with polypeptide over-expression, and thus the level of polypeptide expression must be tested empirically. The instant specification does not provide this additional information, and thus the skilled artisan would need to perform additional experiments. Since the asserted utility for the claimed polypeptides is not in currently available form, the asserted utility is not substantial. Applicants arguments to the contrary fail to meet the urged "more likely than not" standard, but rather fall well within the category that significant further experimentation would be required to determine if the claimed polypeptides have the urged utility, experimentation of the type that was found to be impermissible by the court in *Brenner v. Manson*, 148 U.S.P.Q. 689 (Sup. Ct,.1966).

The effective priority date remains set at 3/30/2000.

Objections and Rejections under 35 U.S.C. §112:

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 132-133 remain rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for the protein of SEQ ID NO: 229 or fragments of such that are usable for making antibodies or have chondrocyte redifferentiation activity, does not reasonably provide enablement for proteins that are encoded by a nucleic acid that is amplified in adenocarcinomas or squamous cell carcinomas of the lung or in adenocarcinomas of the colon. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make or use the invention commensurate in scope with these claims for reasons of record in the previous Office Action. This rejection is maintained for reasons set forth in the Office Action mailed 5/5/2005 and 3/31/2006.

Applicants have presented no new arguments of this rejection. Applicants reiterate their previous arguement that one could go find additional embodiments without undue experimentation. This argument has been fully considered but is not deemed persuasive because it has not been established that the protein of SEQ ID NO: 229 is a diagnostic, much less that there are variants of it that are diagnostic. The recitation of the term "native sequence" is both indefinite and lacks adequate written description. It remains that applicants have found a single nucleic acid, SEQ ID NO: 228, that is found to be aneuploid in a small number of tumor cell lines; there is no enablement that the encoded protein is enabled, nor that there are variants of the protein within the metes and bounds of the claims.

There are no working examples of proteins less than 100% identical SEQ ID NO:229. There is but one function potentially attributed to PRO1111 that meets the requirements of 35 U.S.C. §112, first paragraph: stimulation of chondrocyte redifferentiation. While the specification generally describes properties of cytokines, it is acknowledged that cytokines are diverse in function and structure. The specification does not provide guidance for using polypeptides related to (*i.e.,* 80%-99% identity) but not identical to SEQ ID NO:229 which do not have the single specific disclosed activity potentially shown for PRO1111. The claims are

broad because they do not require the claimed nucleic acid to encode a polypeptide identical to the disclosed sequence and because the claims have no functional limitation.

For these reasons, which include the complexity and unpredictability of the nature of the invention and art in terms of the diversity of proteins and lack of knowledge about function(s) of encompassed polypeptides structurally related to SEQ ID NO:229, the potential one limited working example of PRO1111 polypeptide and its one function, the lack of direction or guidance for using polypeptides that are not identical to SEQ ID NO:229, and the breadth of the claims for structure without function, it would require undue experimentation to use the invention commensurate in scope with the claims.

Claims 132-133 remain rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Further, claims 132-133 are newly amended to remove the recitation that the polypeptide is of a "native sequence". However, they retain the recitation that "the nucleic acid encoding said polypeptide is amplified in adenocarcinomas or squamous cell carcinomas of the lung or in adenocarcinomas of the colon." There is written description of a single species only, SEQ ID NO: 229. There is no written description or conception of any other proteins encoded by nucleic acids that are "amplified in adenocarcinomas or squamous cell carcinomas of the lung or in adenocarcinomas of the colon".

Applicants reiterate their previous traversal that the recitation of a functional property in the claims overcomes the rejection. It is noted that the recitation "the nucleic acid encoding said polypeptide is amplified in adenocarcinomas or squamous cell carcinomas of the lung or in adenocarcinomas of the colon" is not a functional recitation *per se,* but rather a descriptor of where one might encounter the nucleic acids that encode the claimed protein. This argument has been fully considered but is not deemed persuasive because applicants have not established that there is any conception of nucleic acids in a manner commensurate in scope with the claims, and hence of the claimed polypeptides. All applicants have presented is a single nucleic acid found

to be slightly amplified in a small proportion of cancers, and the germ of an idea that there might be variants of the nucleic acid that would be similarly associated. There is no evidence of the actual conception of such nucleic acids, nor is there any evidence of record that they exist. Hence, there is accordingly no written description of the claimed polypeptides, other than the one identified as SEQ ID NO: 229. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016. Accordingly, the rejection is maintained.

Applicants arguments of enablement, that it would not require undue experimentation to determine if other species within the metes and bounds of the claims exist, is not pertinent to this rejection, which is on the grounds of lack of adequate written description. It remains that the specification discloses a single nucleic acid that encodes a single protein; there is no specific conception of how nature might alter either, which is what applicants now seek to claim. All we have here is a wish to know whether other proteins that would be within the metes and bounds of the claims exist, which is not sufficient to meet the written description requirement.

Therefore, proteins comprising the sequence set forth in SEQ ID NO: 229 or active or antigenic fragments thereof but not the full breadth of the claims meet the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 132-133 remain rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The metes and bounds of proteins encoded by nucleic acids" amplified in adenocarcinomas or squamous cell carcinomas of the lung or in adenocarcinomas of the colon ",

as recited in claim 32, cannot be determined, as the specification discloses only the protein of SEQ ID NO: 229, and no other proteins that are 95% identical to such (or 99%) and are encoded by such nucleic acids. Without adequate written description of such, one of ordinary skill in the art would not be able to determine whether a given protein met or did not meet the limitations of the claims. As no sequences having 95 or 99% identity to SEQ ID NO: 229 and that are encoded by nucleic acids amplified in adenocarcinomas or squamous cell carcinomas of the lung or in adenocarcinomas of the colon are described, the metes and bounds of claims 132-133 cannot be determined. It cannot be determined which 95% identical sequences are or are not encoded by such nucleic acids. Were one handed a protein in a test tube, one could not determine whether or not that protein was within the metes and bounds of claim 32. Without a description of a commensurate number of proteins within the metes and bounds of the claim, a given isolated protein cannot be ascribed as being either encoded by such nucleic acids or not. Accordingly, the claim is indefinite. Once a protein is made, it is not possible to determine how it was made, nor its original source. The sequence and structural properties in no way reveal the origin of the molecule or its forebears.

Rejections Over Prior Art:

Priority is set 3/30/00.

A search of the nucleic acid sequence databases revealed the following prior art:

Reference	Date	Author	Identity to SEQ ID NO:228
AI769814	12/21/99	NCI-CGAP	100% to bases 1703-2180
AI435407	3/30/99	NCI-CGAP	99.8% to bases 1743-2185
AI470931	4/13/99	NCI-CGAP	100% to bases 1795-2179
T15752	7/25/96	R. Berry et al.	100% to bases 1870-2184

U.S. Patent Number 6,689,866, SEQ ID NO: 9	3/8/00	Shimkets	99.7% to bases 1-2183
U.S. Patent Number 6,689,866, SEQ ID NO: 31	3/8/00	Shimkets	Encodes XC domain, 100% identity to SEQ ID NO : 229, residues 45-492.

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 124-126, 129 and 132-133 remain rejected under 35 U.S.C. 102(a) as being anticipated by Wang et al., Genbank Accession No. AF196976, cited by applicants. The

sequence of Wang et al. differs from that of SEQ ID NO: 128 by only a single nucleotide, according to applicants alignment. The sequence is described as encoding "Homo sapiens tumor associated protein NAG14". The single nucleotide change is silent, that is, both sequences encode a Valine residue at that position. Cleavage of the signal sequence would automatically occur when expressing the protein in a mammalian cell. Accordingly, the claims are anticipated by Wang et al. Applicants arguments regarding the priority date of the application have been fully considered but are not deemed persuasive for reasons cited above with respect to the priority determination.

Claims 119-123 and 132-133 are rejected under 35 U.S.C. 102(a) as being anticipated by Jacobs et al., Genbank Accession No. AAY28806, cited by applicants. The sequence of Jacobs et al. differs from that of SEQ ID NO: 129 by only a single amino acid, according to applicants alignment. Accordingly, the claims are anticipated by Jacobs et al. Applicants arguments regarding the priority date of the application have been fully considered but are not deemed persuasive for reasons cited above with respect to the priority determination.

Claims 130-133 remain rejected under 35 U.S.C. 102(a) as being anticipated by Jacobs, WO 99/50405. SEQ ID NO: 2 of the publication is 99.7% identical to SEQ ID NO: 229 of the instant application. Fusion proteins, including to epitope tags, are disclosed at page 54. The reference is silent with respect to whether or not the nucleic acid encodes a protein with chondrocyte redifferentiation activity. Since the Office does not have the facilities for examining and comparing applicants' protein with the protein of the prior art, the burden is on applicant to show a novel or unobvious difference between the claimed product and the product of the prior art (i.e., that the protein of the prior art does not possess the same material structural and

functional characteristics of the claimed protein). See In re Best, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and Ex parte Gray, 10 USPQ 2d 1922 1923 (PTO Bd. Pat. App. & Int.).

Applicants arguments regarding the priority date of the application have been fully considered but are not deemed persuasive for reasons cited above with respect to the priority determination.

Claims 124, 127, and 130-133 remain rejected under 35 U.S.C. 102(e) as being anticipated by Shimkets, U.S. Patent Number 6,689,866 or US Patent Application Publication US2003/0054514 A1, or US Patent Application Publication US2003/0003532 A1. The US Patent Application Publications are divisionals of the patent, and differ only in the claims. The '514 publication contains claims to nucleic acids, proteins (see claim 11), and antibodies (see claim 13), and the '532 application contains claims to nucleic acids and vectors. The teachings will be discussed with reference to the issued patent. SEQ ID NO: 9 of the patent is 99.7% identical to SEQ ID NO: 228 of the instant application, at bases 1-2183 (bases 159-2341 of the patent), and encodes a protein 99.2% identical to that of SEQ ID NO: 229. SEQ ID NO: 31 is a fragment of SEQ ID NO: 9, is identified as encoding the extracellular domain (see figures 17A and 17B), which is 100% identical to residues 45-495 of SEQ ID NO: 229. Fusion proteins, including Ig fusions, are disclosed beginning at column 32, line 50.

Accordingly, the claims are anticipated by Shimkets.

Applicants arguments regarding the priority date of the application have been fully considered but are not deemed persuasive for reasons cited above with respect to the priority determination.

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject

> matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 130 and 132-133 remain rejected under 35 U.S.C. 103(a) as being obvious over any one of Loci AI769814, AI435407 , AI470931, or T15752, in view of Sibson et al. For reasons of record in the previous Office action.

The teachings of the primary references are summarized in the Table above. Each has over 99% identity to SEQ ID NO: 228 over the full length of the locus from the database. As sequence identity is calculated relative to the shorter of the two sequences being compared, the proteins encoded by the sequences would meet the limitations of claims 130-132.

Sibson et al. disclose that it is generally useful to place a desired cDNA sequence into an expression vector, host cell, and express the encoded protein, as well as to raise antibodies to proteins encoded by such cDNA's. See pages 8-13. Fusion proteins are disclosed at page 8 as being useful for purification of the encoded protein.

It would have been obvious to the person of ordinary skill in the art at the time the invention was made to use the DNA's disclosed by any one of the primary references to express and then isolate the encoded polypeptide as taught by Sibson et al. in view of Sibson et al.'s suggestion that it would be desirable to do so, as cited above.

Applicants argument that ESTs are not enabling disclosures since they provide no utility has been fully considered but is not deemed persuasive. Utility as defined by 35 U.S.C. §101 is not required for a finding of obviousness. The EST disclosures disclose and enable one of

ordinary skill in the art to make the DNAs disclosed therein. Sibson provides the motivation to express such sequences to make protein. Accordingly, the invention as claimed is *prima facie* obvious.

Applicants argue that the references have not taught how to derive the rest of the DNA sequence. This argument has been fully considered but is not deemed persuasive because as stated in the rejection, as sequence identity is calculated relative to the shorter of the two sequences being compared, the proteins encoded by the sequences would meet the limitations of claims 130-132. Applicants also argue at page 18 of the response filed 9/29/2006 that "the USPTO acknowledges that EST sequences are not enabling". This argument has been fully considered but is not deemed persuasive because applicants have failed to point out where, when and under what circumstances the USPTO has found such. Each case must be examined on its own merits. In this case, the sequence disclosures disclose the nucleic acids needed to make the claimed proteins. Sibson provides means and motivation to express any given nucleic acid sequence to make the protein encoded thereby. Hence, the cited references, in the combination in which they are cited, provide the materials, methods and motivation to arrive at the claimed invention. That is as much enablement as is required.

Applicants arguments regarding the priority date of the application have been fully considered but are not deemed persuasive for reasons cited above with respect to the priority determination.

Claim 131 remains rejected over any one of Loci AI769814, AI435407 , AI470931, or T15752, in view of Sibson et al. and further in view of Capon et al., U.S. Patent Number 5,116,964 for reasons of record in the previous Office action. Applicants have presented no further argument of this rejection.

Claims 130 and 131 remain rejected under 35 U.S.C. 103(a) as being unpatentable over Wang et al., Genbank Accession No. AF196976, cited by applicants, in view of Capon et al., U.S. Patent Number 5,116,964 for reasons of record in the previous Office action for reasons

cited with respect to claim 131 in the rejection over one of Loci AI769814, AI435407 , AI470931, or T15752, in view of Sibson et al. and further in view of Capon et al., U.S. Patent Number 5,116,964 in the previous Office Action.

Advisory Information:

Claims 125 and 129 remain objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

No claim is allowed.

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL.** See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the Examiner should be directed to Lorraine M. Spector. Dr. Spector can normally be reached Monday through Friday, 9:00 A.M. to 3:00 P.M. at telephone number 571-272-0893.

If attempts to reach the Examiner by telephone are unsuccessful, please contact the Examiner's supervisor, Ms. Brenda Brumback, at telephone number 571-272-0961.

Certain papers related to this application may be submitted to Technology Center 1600 by facsimile transmission The faxing of such papers must conform with the notices published in the Official Gazette, 1156 OG 61 (November 16, 1993) and 1157 OG 94 (December 28, 1993)

(see 37 C.F.R. § 1.6(d)). NOTE: If Applicant does submit a paper by fax, the original signed copy should be retained by applicant or applicant's representative. NO DUPLICATE COPIES SHOULD BE SUBMITTED so as to avoid the processing of duplicate papers in the Office.

Official papers filed by fax should be directed to 571-273-8300. Faxed draft or informal communications with the examiner should be directed to ***571-273-0893.***

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Lorraine Spector

Lorraine Spector, Ph.D.
Primary Examiner